RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: ______

Source:

Date Processed by STIC:

ENTERED

CRF Errors Edited by the STIC Systems Branch

Pi-1

Serial	Number: 10/590, 122	CRF Edit Date: 9/6/0 C Edited by: Z
	Realigned nucleic acid/amino acid numbers/text text "wrapped" to the next line	in cases where the sequence
	Corrected the SEQ ID NO. Sequence numbers e	edited were:
	Inserted or corrected a nucleic number at the end NO's edited:	d of a nucleic line. SEQ ID
	Deleted: invalid beginning/end-of-file text;	page numbers
	Inserted mandatory headings/numeric identifiers	s, specifically:
·····	Moved responses to same line as heading/numeri	c identifier, specifically:
	Other:	

Revised 09/09/2003



IFWP

RAW SEQUENCE LISTING DATE: 09/06/2006
PATENT APPLICATION: US/10/590,122 TIME: 13:26:46

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\09052006\J590122.raw

3 <110> APPLICANT: Yamakawa, Naomi 5 <120> TITLE OF INVENTION: DNA array for analyzing DNA methylation, process for manufacturing the same, and method for analyzing DNA methylation 6 8 <130> FILE REFERENCE: 2352.016 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/590,122 C--> 10 <141> CURRENT FILING DATE: 2006-08-18 10 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/002490 11 <151> PRIOR FILING DATE: 2005-02-17 13 <160> NUMBER OF SEQ ID NOS: 4 15 <170> SOFTWARE: PatentIn version 3.1 17 <210> SEQ ID NO: 1 18 <211> LENGTH: 20 19 <212> TYPE: DNA 20 <213> ORGANISM: Homo sapiens 22 <400> SEQUENCE: 1 23 attcgaaccc agtggaatca 20 26 <210> SEQ ID NO: 2 27 <211> LENGTH: 20 28 <212> TYPE: DNA 29 <213> ORGANISM: Homo sapiens 31 <400> SEQUENCE: 2 32 ctagcctgga gttgctaggg 20 35 <210> SEQ ID NO: 3 36 <211> LENGTH: 20 37 <212> TYPE: DNA 38 <213 > ORGANISM: Homo sapiens 40 <400> SEQUENCE: 3 41 gaactgcaaa gcacctgtga 20 44 <210> SEQ ID NO: 4 45 <211> LENGTH: 19 46 <212> TYPE: DNA 47 <213> ORGANISM: Homo sapiens 49 <400> SEQUENCE: 4 50 gggctggagt ctgaactga 19

VERIFICATION SUMMARY

DATE: 09/06/2006

PATENT APPLICATION: US/10/590,122

TIME: 13:26:47

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\09052006\J590122.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

Raw Sequence Listing before editing (for reference only)



IFWP

RAW SEQUENCE LISTING

DATE: 08/28/2006

PATENT APPLICATION: US/10/590,122

TIME: 09:52:57

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\08282006\J590122.raw

3 <110> APPLICANT: Yamakawa, Naomi

5 <120> TITLE OF INVENTION: DNA array for analyzing DNA methylation, process for

manufacturing the

same, and method for analyzing DNA methylation

8 <130> FILE REFERENCE: 2352.016

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/590,122

C--> 10 <141> CURRENT FILING DATE: 2006-08-18

10 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/002490

11 <151> PRIOR FILING DATE: 2005-02-17

13 <160> NUMBER OF SEQ ID NOS: 4

15 <170> SOFTWARE: PatentIn version 3.1

Dres Not Comply Corrected Diskette Needed

ERRORED SEQUENCES

44 <210> SEQ ID NO: 4

45 <211> LENGTH: 19

46 <212> TYPE: DNA

47 <213> ORGANISM: Homo sapiens

49 <400> SEQUENCE: 4

50 gggctggagt ctqaactga

19

VERIFICATION SUMMARYDATE: 08/28/2006PATENT APPLICATION: US/10/590,122TIME: 09:52:58

Input Set : A:\PTO.RJ.txt

3. . S

Output Set: N:\CRF4\08282006\J590122.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:57 M:254 E: No. of Bases conflict, this line has no nucleotides.